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Anderson et al.

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(A) identifying a putative polypeptide domain that properly folds into a stable polypeptide domain of 50 to 300 amino acids;

(B) determining three dimensional structure of the stable polypeptide domain;

(C) comparing the determined three dimensional structure of the stable polypeptide domain to known three-dimensional structures in a protein data bank, wherein said comparison identifies known structures within said protein data bank that are homologous to the determined three dimensional structure; and

(D) correlating a biochemical function corresponding to the identified homologous structure to a biochemical function for the stable polypeptide domain.

REMARKS

Claims 1-17 are pending in the instant application. Claims 1-17 have been rejected. Claim 1 has been amended. No new matter has been added by these amendments. Reconsideration is respectfully requested in light of these amendments and the following remarks.